

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/030, 194 B  
Source: JFW16  
Date Processed by STIC: 11/13/2006

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 11/13/2006

PATENT APPLICATION: US/10/030,194B

TIME: 12:30:18

Input Set : A:\218874US0PCT.txt

Output Set: N:\CRF4\11132006\J030194B.raw

3 <110> APPLICANT: RENARD, MICHEL  
 4 DELOURME, REGINE  
 5 BARRET, PIERRE  
 6 BRUNEL, DOMINIQUE  
 7 FROGER, NICOLE  
 8 TANGUY, XAVIER  
 10 <120> TITLE OF INVENTION: MUTANT GENE OF THE GRAS FAMILY AND PLANTS WITH REDUCED  
 11 DEVELOPMENT CONTAINING SAID MUTANT GENE  
 13 <130> FILE REFERENCE: 218874US0PCT  
 15 <140> CURRENT APPLICATION NUMBER: 10/030,194B  
 C--> 16 <141> CURRENT FILING DATE: 2002-08-15  
 18 <150> PRIOR APPLICATION NUMBER: PCT/FR00/02216  
 19 <151> PRIOR FILING DATE: 2000-08-02  
 21 <150> PRIOR APPLICATION NUMBER: FR 9910023  
 22 <151> PRIOR FILING DATE: 1999-08-02  
 24 <160> NUMBER OF SEQ ID NOS: 7  
 26 <170> SOFTWARE: PatentIn version 3.3  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 1779  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: Brassica napus  
 34 <220> FEATURE:  
 35 <221> NAME/KEY: CDS  
 36 <222> LOCATION: (60)..(1778)  
 38 <400> SEQUENCE: 1  
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 41 atg aag agg gat ctt cat cag ttc caa ggt ccc aac cac ggg aca tca 107  
 42 Met Lys Arg Asp Leu His Gln Phe Gln Gly Pro Asn His Gly Thr Ser  
 43 1 5 10 15  
 45 atc gcc ggt tct tcc act tct tcc cct gcg gtg ttt ggt aaa gac aag 155  
 46 Ile Ala Gly Ser Ser Thr Ser Ser Pro Ala Val Phe Gly Lys Asp Lys  
 47 20 25 30  
 49 atg atg atg gtc aaa gaa gaa gaa gac gac gag ctt cta gga gtc ttg 203  
 50 Met Met Met Val Lys Glu Glu Glu Asp Asp Glu Leu Leu Gly Val Leu  
 51 35 40 45  
 53 ggt tac aag gtt agg tct tcg gag atg gct gag gtt gcg ttg aaa ctc 251  
 54 Gly Tyr Lys Val Arg Ser Ser Glu Met Ala Glu Val Ala Leu Lys Leu  
 55 50 55 60  
 57 gag cag ctt gag acg atg atg ggt aac gct caa gaa gac ggt tta gct 299  
 58 Glu Gln Leu Glu Thr Met Met Gly Asn Ala Gln Glu Asp Gly Leu Ala  
 59 65 70 75 80  
 61 cac ctc gcg acg gat act gtt cat tac aac ccc gct gag ctt tac tcg 347  
 62 His Leu Ala Thr Asp Thr Val His Tyr Asn Pro Ala Glu Leu Tyr Ser

CP2-67

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63		85		90		95		
65	tgg ctt gat aac atg ctc acg gag ctt aac cca ccc gct gca acg acc							395
66	Trp Leu Asp Asn Met Leu Thr Glu Leu Asn Pro Pro Ala Ala Thr Thr							
67		100		105		110		
69	gga tct aac gct ttg aac ccg gag att aat aat aat aat aat aac tcg							443
70	Gly Ser Asn Ala Leu Asn Pro Glu Ile Asn Asn Asn Asn Asn Asn Ser							
71		115		120		125		
73	ttt ttc acc gga ggc gac ctc aaa gcg att cct gga aac gcg gtt tgt							491
74	Phe Phe Thr Gly Gly Asp Leu Lys Ala Ile Pro Gly Asn Ala Val Cys							
75		130		135		140		
77	cgc aga tct aat cag ttc gcg ttt gcg gtt gat tcg tcg agt aat aag							539
78	Arg Arg Ser Asn Gln Phe Ala Phe Ala Val Asp Ser Ser Ser Asn Lys							
79	145		150		155		160	
81	cgt ttg aaa ccg tcc tcg agc cct gat tcg atg gtt aca tct cca tca							587
82	Arg Leu Lys Pro Ser Ser Ser Pro Asp Ser Met Val Thr Ser Pro Ser							
83		165		170		175		
85	cct gct gga gtt ata gga acg acg gtt aca acc gtg acc gag tca act							635
86	Pro Ala Gly Val Ile Gly Thr Thr Val Thr Thr Val Thr Glu Ser Thr							
87		180		185		190		
89	cgt cct tta atc ctg gtc gac tcg cag gac aac gga gtg cgt cta gtc							683
90	Arg Pro Leu Ile Leu Val Asp Ser Gln Asp Asn Gly Val Arg Leu Val							
91		195		200		205		
93	cac gcg ctt atg gcc tgc gct gaa gcc gtg cag agc agc aac ttg act							731
94	His Ala Leu Met Ala Cys Ala Glu Ala Val Gln Ser Ser Asn Leu Thr							
95		210		215		220		
97	cta gcg gag gct ctc gtt aag cag att ggt ttc ttg gcc gtc tct caa							779
98	Leu Ala Glu Ala Leu Val Lys Gln Ile Gly Phe Leu Ala Val Ser Gln							
99	225		230		235		240	
101	gcc gga gcc atg agg aaa gtc gcc acg tac ttc gcc gaa gct ctc gcg							827
102	Ala Gly Ala Met Arg Lys Val Ala Thr Tyr Phe Ala Glu Ala Leu Ala							
103		245		250		255		
105	cgg agg atc tac cgc ctc tct ccg ccg cag acg cag atc gat cac tct							875
106	Arg Arg Ile Tyr Arg Leu Ser Pro Pro Gln Thr Gln Ile Asp His Ser							
107		260		265		270		
109	tta tcc gat act ctc cag atg cac ttc tac gag act tgc cct tac ctc							923
110	Leu Ser Asp Thr Leu Gln Met His Phe Tyr Glu Thr Cys Pro Tyr Leu							
111		275		280		285		
113	aag ttc gct cac ttc acg gcg aat cag gcg att ctc gag gct ttc gaa							971
114	Lys Phe Ala His Phe Thr Ala Asn Gln Ala Ile Leu Glu Ala Phe Glu							
115		290		295		300		
117	ggg aag aag aga gtc cac gtc atc gat ttc tcg atg aac caa ggg ctt							1019
118	Gly Lys Lys Arg Val His Val Ile Asp Phe Ser Met Asn Gln Gly Leu							
119	305		310		315		320	
121	cag tgg ccc gcg ctt atg caa gcc ctt gcg ttg agg gaa gga ggt cct							1067
122	Gln Trp Pro Ala Leu Met Gln Ala Leu Ala Leu Arg Glu Gly Gly Pro							
123		325		330		335		
125	ccg agt ttc agg tta acc gga att ggt cct ccc gcg gcg gat aac tcc							1115
126	Pro Ser Phe Arg Leu Thr Gly Ile Gly Pro Pro Ala Ala Asp Asn Ser							
127		340		345		350		

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129 gat cat ctc cat gaa gtt gga tgt aag ttg gct cag ctc gcg gag gcg      1163
130 Asp His Leu His Glu Val Gly Cys Lys Leu Ala Gln Leu Ala Glu Ala
131      355      360      365
133 att cac gtc gag ttt gag tat cgt ggc ttt gtt gct aat agc tta gct      1211
134 Ile His Val Glu Phe Glu Tyr Arg Gly Phe Val Ala Asn Ser Leu Ala
135      370      375      380
137 gat ctt gat gcc tcg atg ctt gag ctt aga ccg agt gaa acc gaa gct      1259
138 Asp Leu Asp Ala Ser Met Leu Glu Leu Arg Pro Ser Glu Thr Glu Ala
139 385      390      395      400
141 gtg gcg gtt aac tct gtt ttc gag ctc cac aag ctc cta ggc cgt acc      1307
142 Val Ala Val Asn Ser Val Phe Glu Leu His Lys Leu Leu Gly Arg Thr
143      405      410      415
145 ggt ggg ata gag aaa gtc ttc ggc gtt gtg aaa cag att aaa ccg gtg      1355
146 Gly Gly Ile Glu Lys Val Phe Gly Val Val Lys Gln Ile Lys Pro Val
147      420      425      430
149 att ttc acg gtt gtt gag caa gaa tcg aat cat aac ggt ccg gtt ttc      1403
150 Ile Phe Thr Val Val Glu Gln Glu Ser Asn His Asn Gly Pro Val Phe
151      435      440      445
153 tta gac cgg ttt act gaa tcg ctg cat tat tat tcg acg ttg ttt gat      1451
154 Leu Asp Arg Phe Thr Glu Ser Leu His Tyr Tyr Ser Thr Leu Phe Asp
155      450      455      460
157 tcc ttg gaa ggt gct ccg agt agc caa gat aaa gtt atg tcg gaa gtt      1499
158 Ser Leu Glu Gly Ala Pro Ser Ser Gln Asp Lys Val Met Ser Glu Val
159 465      470      475      480
161 tat tta ggg aaa cag att tgc aat ctg gtg gct tgc gaa ggt ccg gac      1547
162 Tyr Leu Gly Lys Gln Ile Cys Asn Leu Val Ala Cys Glu Gly Pro Asp
163      485      490      495
165 cgt gtt gag aga cat gag acg ctg agt caa tgg tcg aac ccg ttc ggt      1595
166 Arg Val Glu Arg His Glu Thr Leu Ser Gln Trp Ser Asn Arg Phe Gly
167      500      505      510
169 tcg tcc ggt ttt gcg ccg gcg cat ctc ggg tct aac gcg ttt aag caa      1643
170 Ser Ser Gly Phe Ala Pro Ala His Leu Gly Ser Asn Ala Phe Lys Gln
171      515      520      525
173 gcg agt acg ctt ttg gct ttg ttt aat gga ggc gaa ggt tat cgt gtg      1691
174 Ala Ser Thr Leu Leu Ala Leu Phe Asn Gly Gly Glu Gly Tyr Arg Val
175      530      535      540
177 gag gag aat aat ggg tgt ttg atg ttg agt tgg cac act cga ccg ctc      1739
178 Glu Glu Asn Asn Gly Cys Leu Met Leu Ser Trp His Thr Arg Pro Leu
179 545      550      555      560
181 ata acc acc tcc gct tgg aag ctc tcg gcg gtg cac tga g      1779
182 Ile Thr Thr Ser Ala Trp Lys Leu Ser Ala Val His
183      565      570
186 <210> SEQ ID NO: 2
187 <211> LENGTH: 572
188 <212> TYPE: PRT
189 <213> ORGANISM: Brassica napus
191 <400> SEQUENCE: 2
193 Met Lys Arg Asp Leu His Gln Phe Gln Gly Pro Asn His Gly Thr Ser
194 1      5      10      15

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198      20      25      30
201 Met Met Met Val Lys Glu Glu Glu Asp Asp Glu Leu Leu Gly Val Leu
202      35      40      45
205 Gly Tyr Lys Val Arg Ser Ser Glu Met Ala Glu Val Ala Leu Lys Leu
206      50      55      60
209 Glu Gln Leu Glu Thr Met Met Gly Asn Ala Gln Glu Asp Gly Leu Ala
210 65      70      75      80
213 His Leu Ala Thr Asp Thr Val His Tyr Asn Pro Ala Glu Leu Tyr Ser
214      85      90      95
217 Trp Leu Asp Asn Met Leu Thr Glu Leu Asn Pro Pro Ala Ala Thr Thr
218      100     105     110
221 Gly Ser Asn Ala Leu Asn Pro Glu Ile Asn Asn Asn Asn Asn Ser
222      115     120     125
225 Phe Phe Thr Gly Gly Asp Leu Lys Ala Ile Pro Gly Asn Ala Val Cys
226      130     135     140
229 Arg Arg Ser Asn Gln Phe Ala Phe Ala Val Asp Ser Ser Ser Asn Lys
230 145     150     155     160
233 Arg Leu Lys Pro Ser Ser Ser Pro Asp Ser Met Val Thr Ser Pro Ser
234      165     170     175
237 Pro Ala Gly Val Ile Gly Thr Thr Val Thr Thr Val Thr Glu Ser Thr
238      180     185     190
241 Arg Pro Leu Ile Leu Val Asp Ser Gln Asp Asn Gly Val Arg Leu Val
242      195     200     205
245 His Ala Leu Met Ala Cys Ala Glu Ala Val Gln Ser Ser Asn Leu Thr
246      210     215     220
249 Leu Ala Glu Ala Leu Val Lys Gln Ile Gly Phe Leu Ala Val Ser Gln
250 225     230     235     240
253 Ala Gly Ala Met Arg Lys Val Ala Thr Tyr Phe Ala Glu Ala Leu Ala
254      245     250     255
257 Arg Arg Ile Tyr Arg Leu Ser Pro Pro Gln Thr Gln Ile Asp His Ser
258      260     265     270
261 Leu Ser Asp Thr Leu Gln Met His Phe Tyr Glu Thr Cys Pro Tyr Leu
262      275     280     285
265 Lys Phe Ala His Phe Thr Ala Asn Gln Ala Ile Leu Glu Ala Phe Glu
266      290     295     300
269 Gly Lys Lys Arg Val His Val Ile Asp Phe Ser Met Asn Gln Gly Leu
270 305     310     315     320
273 Gln Trp Pro Ala Leu Met Gln Ala Leu Ala Leu Arg Glu Gly Gly Pro
274      325     330     335
277 Pro Ser Phe Arg Leu Thr Gly Ile Gly Pro Pro Ala Ala Asp Asn Ser
278      340     345     350
281 Asp His Leu His Glu Val Gly Cys Lys Leu Ala Gln Leu Ala Glu Ala
282      355     360     365
285 Ile His Val Glu Phe Glu Tyr Arg Gly Phe Val Ala Asn Ser Leu Ala
286      370     375     380
289 Asp Leu Asp Ala Ser Met Leu Glu Leu Arg Pro Ser Glu Thr Glu Ala
290 385     390     395     400
293 Val Ala Val Asn Ser Val Phe Glu Leu His Lys Leu Leu Gly Arg Thr

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294          405          410          415
297 Gly Gly Ile Glu Lys Val Phe Gly Val Val Lys Gln Ile Lys Pro Val
298          420          425          430
301 Ile Phe Thr Val Val Glu Gln Glu Ser Asn His Asn Gly Pro Val Phe
302          435          440          445
305 Leu Asp Arg Phe Thr Glu Ser Leu His Tyr Tyr Ser Thr Leu Phe Asp
306          450          455          460
309 Ser Leu Glu Gly Ala Pro Ser Ser Gln Asp Lys Val Met Ser Glu Val
310 465          470          475          480
313 Tyr Leu Gly Lys Gln Ile Cys Asn Leu Val Ala Cys Glu Gly Pro Asp
314          485          490          495
317 Arg Val Glu Arg His Glu Thr Leu Ser Gln Trp Ser Asn Arg Phe Gly
318          500          505          510
321 Ser Ser Gly Phe Ala Pro Ala His Leu Gly Ser Asn Ala Phe Lys Gln
322          515          520          525
325 Ala Ser Thr Leu Leu Ala Leu Phe Asn Gly Gly Glu Gly Tyr Arg Val
326          530          535          540
329 Glu Glu Asn Asn Gly Cys Leu Met Leu Ser Trp His Thr Arg Pro Leu
330 545          550          555          560
333 Ile Thr Thr Ser Ala Trp Lys Leu Ser Ala Val His
334          565          570
337 <210> SEQ ID NO: 3
338 <211> LENGTH: 1779
339 <212> TYPE: DNA
340 <213> ORGANISM: Brassica napus
343 <220> FEATURE:
344 <221> NAME/KEY: CDS
345 <222> LOCATION: (60)..(1778)
347 <400> SEQUENCE: 3
348 caaccagaa caaaaccaga cccgatctgag agattaacta tatcttaacc agatcagaa      59
350 atg aag agg gat ctt cat cag ttc caa ggt ccc aac cac ggg aca tca      107
351 Met Lys Arg Asp Leu His Gln Phe Gln Gly Pro Asn His Gly Thr Ser
352 1          5          10          15
354 atc gcc ggt tct tcc act tct tcc cct gcg gtg ttt ggt aaa gac aag      155
355 Ile Ala Gly Ser Ser Thr Ser Ser Pro Ala Val Phe Gly Lys Asp Lys
356          20          25          30
358 atg atg atg gtc aaa gaa gaa gaa gac gac gag ctt cta gga gtc ttg      203
359 Met Met Met Val Lys Glu Glu Glu Asp Asp Glu Leu Leu Gly Val Leu
360          35          40          45
362 ggt tac aag gtt agg tct tcg gag atg gct gag gtt gcg ttg aaa ctc      251
363 Gly Tyr Lys Val Arg Ser Ser Glu Met Ala Glu Val Ala Leu Lys Leu
364          50          55          60
366 gag cag ctt gag acg atg atg ggt aac gct caa gaa gac ggt tta gct      299
367 Glu Gln Leu Glu Thr Met Met Gly Asn Ala Gln Glu Asp Gly Leu Ala
368 65          70          75          80
370 cac ctc gcg acg gat act gtt cat tac aac ccc gct gag ctt tac tcg      347
371 His Leu Ala Thr Asp Thr Val His Tyr Asn Pro Ala Glu Leu Tyr Ser
372          85          90          95
374 tgg ctt gat aac atg ctc acg gag ctt aac cca ccc gct gca acg acc      395

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/030,194B

DATE: 11/13/2006  
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Input Set : A:\218874US0PCT.txt  
Output Set: N:\CRF4\11132006\J030194B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 3  
Seq#:6; Xaa Pos. 3,6  
Seq#:7; Xaa Pos. 3,6

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/030,194B

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Input Set : A:\218874US0PCT.txt

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:662 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0

L:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0

L:712 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0